



SEQUENCE LISTING

<110> GLUCKSMANN, MARIA ALEXANDRA

<120> 93870, A HUMAN G-PROTEIN COUPLED
RECEPTOR AND USES THEREFOR

<130> MPI2001-021P1RCP1 (M)

<140> 10/085,233

<141> 2002-02-28

<150> 60/272,677

<151> 2001-03-01

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1684

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147)...(1085)

<223> n at position 1384 can be any
nucleotide

<400> 1

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tggaagtgtg agactggata agagatgctc agctaaggga gttcctggat ggcctttaga 120
ttgatacacc aatcctctga aattgc atg caa aaa tgt gac ttc cca agt atg 173
Met Gln Lys Cys Asp Phe Pro Ser Met
1 5
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cct ggc cac aat acc tcc agg aat tcc tct tgc gat cct ata gtg aca 221
Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr
10 15 20 25
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ccc cac tta atc agc ctc tac ttc ata gtg ctt att ggc ggg ctg gtg 269
Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val
30 35 40
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ggg gtc att tcc att ctt ttc ctc ctg gtg aaa atg aac acc cgg tca 317
Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser
45 50 55
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gtg acc acc atg gcg gtc att aac ttg gtg gtg gtc cac agc gtt ttt 365
Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val Phe
60 65 70
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ctg ctg aca gtg cca ttt cgc ttg acc tac ctc atc aag aag act tgg 413
Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp
75 80 85
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atg ttt ggg ctg ccc ttc tgc aaa ttt gtg agt gcc atg ctg cac atc 461
Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile
90 95 100 105
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cac atg tac ctc acg ttc cta ttc tat gtg gtg atc ctg gtc acc aga 509
His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr Arg
110 115 120
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tac ctc atc ttc ttc aag tgc aaa gac aaa gtg gaa ttc tac aga aaa 557
Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg Lys
125 130 135

ctg cat gct gtg gct gcc agt gct ggc atg tgg acg ctg gtg att gtc 605
Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile Val
140 145 150

att gtg gta ccc ctg gtt gtc tcc cgg tat gga atc cat gag gaa tac 653
Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu Tyr
155 160 165

aat gag gag cac tgt ttt aaa ttt cac aaa gag ctt gct tac aca tat 701
Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr Tyr
170 175 180 185

gtg aaa atc atc aac tat atg ata gtc att ttt gtc ata gcc gtt gct 749
Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val Ala
190 195 200

gtg att ctg ttg gtc ttc cag gtc ttc atc att atg ttg atg gtg cag 797
Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val Gln
205 210 215

aag cta cgc cac tct tta cta tcc cac cag gag ttc tgg gct cag ctg 845
Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln Leu
220 225 230

aaa aac cta ttt ttt ata ggg gtc atc ctt gtt tgt ttc ctt ccc tac 893
Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro Tyr
235 240 245

cag ttc ttt agg atc tat tac ttg aat gtt gtg acg cat tcc aat gcc 941
Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn Ala
250 255 260 265

tgt agc agc aag gtt gca ttt tat aac gaa atc ttc ttg agt gta aca 989
Cys Ser Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val Thr
270 275 280

gca att agc tgc tat gat ttg ctt ctc ttt gtc ttt ggg gga agc cat 1037
Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser His
285 290 295

tgg ttt aag caa aag ata att ggc tta tgg aat tgt gtt ttg tgc cgt 1085
Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys Arg
300 305 310

tagccacaaa ctacagtatt catatttgct tcctttatat tgggaataaa atgggtatag 1145
gggaggttaag aatggtatatt cattacttga tcaaaaccat gccttgatgt acccaaaaca 1205
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agtgatggcc gtacaaagac cagtgttggt gaatccacct ggagttgcaa tattacatta 1325
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gagtttcatt agctcattct aagttcctct gtttgaagca tgggtctctta ggttttggac 1445
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ccaccagct ccaaagacac aaactctcct tcgctaacca gggttagatgt cccattcatc 1565
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<210> 2
<211> 313
<212> PRT
<213> Homo sapiens

<400> 2
Met Gln Lys Cys Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg
1 5 10 15
Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr
20 25 30

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Phe Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe
 35 40 45
 Leu Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile
 50 55 60
 Asn Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg
 65 70 75 80
 Leu Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys
 85 90 95
 Lys Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu
 100 105 110
 Phe Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys
 115 120 125
 Lys Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser
 130 135 140
 Ala Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val
 145 150 155 160
 Ser Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys
 165 170 175
 Phe His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met
 180 185 190
 Ile Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln
 195 200 205
 Val Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu
 210 215 220
 Ser His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly
 225 230 235 240
 Val Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr
 245 250 255
 Leu Asn Val Val Thr His Ser Asn Ala Cys Ser Ser Lys Val Ala Phe
 260 265 270
 Tyr Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu
 275 280 285
 Leu Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile
 290 295 300
 Gly Leu Trp Asn Cys Val Leu Cys Arg
 305 310

<210> 3
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

<400> 3
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 aat tcc tct tgc gat cct ata gtg aca ccc cac tta atc agc ctc tac 96
 Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr
 20 25 30
 ttc ata gtg ctt att ggc ggg ctg gtg ggt gtc att tcc att ctt ttc 144
 Phe Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe
 35 40 45
 ctc ctg gtg aaa atg aac acc cgg tca gtg acc acc atg gcg gtc att 192
 Leu Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile
 50 55 60
 aac ttg gtg gtg gtc cac agc gtt ttt ctg ctg aca gtg cca ttt cgc 240
 Asn Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg
 65 70 75 80
 ttg acc tac ctc atc aag aag act tgg atg ttt ggg ctg ccc ttc tgc 288
 Leu Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys

85										90					95					
aaa	ttt	gtg	agt	gcc	atg	ctg	cac	atc	cac	atg	tac	ctc	acg	ttc	cta	336				
Lys	Phe	Val	Ser	Ala	Met	Leu	His	Ile	His	Met	Tyr	Leu	Thr	Phe	Leu					
			100					105					110							
ttc	tat	gtg	gtg	atc	ctg	gtc	acc	aga	tac	ctc	atc	ttc	ttc	aag	tgc	384				
Phe	Tyr	Val	Val	Ile	Leu	Val	Thr	Arg	Tyr	Leu	Ile	Phe	Phe	Lys	Cys					
		115					120					125								
aaa	gac	aaa	gtg	gaa	ttc	tac	aga	aaa	ctg	cat	gct	gtg	gct	gcc	agt	432				
Lys	Asp	Lys	Val	Glu	Phe	Tyr	Arg	Lys	Leu	His	Ala	Val	Ala	Ala	Ser					
	130					135					140									
gct	ggc	atg	tgg	acg	ctg	gtg	att	gtc	att	gtg	gta	ccc	ctg	gtt	gtc	480				
Ala	Gly	Met	Trp	Thr	Leu	Val	Ile	Val	Ile	Val	Val	Pro	Leu	Val	Val					
145					150					155					160					
tcc	cgg	tat	gga	atc	cat	gag	gaa	tac	aat	gag	gag	cac	tgt	ttt	aaa	528				
Ser	Arg	Tyr	Gly	Ile	His	Glu	Glu	Tyr	Asn	Glu	Glu	His	Cys	Phe	Lys					
				165					170					175						
ttt	cac	aaa	gag	ctt	gct	tac	aca	tat	gtg	aaa	atc	atc	aac	tat	atg	576				
Phe	His	Lys	Glu	Leu	Ala	Tyr	Thr	Tyr	Val	Lys	Ile	Ile	Asn	Tyr	Met					
			180					185					190							
ata	gtc	att	ttt	gtc	ata	gcc	gtt	gct	gtg	att	ctg	ttg	gtc	ttc	cag	624				
Ile	Val	Ile	Phe	Val	Ile	Ala	Val	Ala	Val	Ile	Leu	Leu	Val	Phe	Gln					
		195					200					205								
gtc	ttc	atc	att	atg	ttg	atg	gtg	cag	aag	cta	cgc	cac	tct	tta	cta	672				
Val	Phe	Ile	Ile	Met	Leu	Met	Val	Gln	Lys	Leu	Arg	His	Ser	Leu	Leu					
	210					215					220									
tcc	cac	cag	gag	ttc	tgg	gct	cag	ctg	aaa	aac	cta	ttt	ttt	ata	ggg	720				
Ser	His	Gln	Glu	Phe	Trp	Ala	Gln	Leu	Lys	Asn	Leu	Phe	Phe	Ile	Gly					
225					230					235					240					
gtc	atc	ctt	gtt	tgt	ttc	ctt	ccc	tac	cag	ttc	ttt	agg	atc	tat	tac	768				
Val	Ile	Leu	Val	Cys	Phe	Leu	Pro	Tyr	Gln	Phe	Phe	Arg	Ile	Tyr	Tyr					
				245					250					255						
ttg	aat	gtt	gtg	acg	cat	tcc	aat	gcc	tgt	agc	agc	aag	gtt	gca	ttt	816				
Leu	Asn	Val	Val	Thr	His	Ser	Asn	Ala	Cys	Ser	Ser	Lys	Val	Ala	Phe					
			260					265					270							
tat	aac	gaa	atc	ttc	ttg	agt	gta	aca	gca	att	agc	tgc	tat	gat	ttg	864				
Tyr	Asn	Glu	Ile	Phe	Leu	Ser	Val	Thr	Ala	Ile	Ser	Cys	Tyr	Asp	Leu					
		275					280					285								
ctt	ctc	ttt	gtc	ttt	ggg	gga	agc	cat	tgg	ttt	aag	caa	aag	ata	att	912				
Leu	Leu	Phe	Val	Phe	Gly	Gly	Ser	His	Trp	Phe	Lys	Gln	Lys	Ile	Ile					
	290					295					300									
ggc	tta	tgg	aat	tgt	gtt	ttg	tgc	cgt								939				
Gly	Leu	Trp	Asn	Cys	Val	Leu	Cys	Arg												
305					310															
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<211>	356																			
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			20					25					30							
Phe	Gly	Ile	Thr	Val	Pro	Thr	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Ile					

		35					40					45			
Gly	Val	Ile	Gly	His	Val	Leu	Val	Val	Leu	Val	Leu	Ile	Gln	His	Lys
	50					55					60				
Arg	Leu	Arg	Asn	Met	Thr	Ser	Ile	Tyr	Leu	Phe	Asn	Leu	Ala	Ile	Ser
65					70					75					80
Asp	Leu	Val	Phe	Leu	Ser	Thr	Leu	Pro	Phe	Trp	Val	Asp	Tyr	Ile	Met
				85					90					95	
Lys	Gly	Asp	Trp	Ile	Phe	Gly	Asn	Ala	Met	Cys	Lys	Phe	Val	Ser	Gly
			100					105					110		
Phe	Tyr	Tyr	Leu	Gly	Leu	Tyr	Ser	Asp	Met	Phe	Phe	Ile	Thr	Leu	Leu
			115				120					125			
Thr	Ile	Asp	Arg	Tyr	Leu	Ala	Val	Val	His	Val	Val	Phe	Ala	Leu	Arg
	130					135					140				
Ala	Arg	Thr	Val	Thr	Phe	Gly	Ile	Ile	Ser	Ser	Ile	Ile	Thr	Trp	Val
145					150					155					160
Leu	Ala	Ala	Leu	Val	Ser	Ile	Pro	Cys	Leu	Tyr	Val	Phe	Lys	Ser	Gln
				165					170					175	
Met	Glu	Phe	Thr	Tyr	His	Thr	Cys	Arg	Ala	Ile	Leu	Pro	Arg	Lys	Ser
			180				185						190		
Leu	Ile	Arg	Phe	Leu	Arg	Phe	Gln	Ala	Leu	Thr	Met	Asn	Ile	Leu	Gly
		195					200					205			
Leu	Ile	Leu	Pro	Leu	Leu	Ala	Met	Ile	Ile	Cys	Tyr	Thr	Arg	Ile	Ile
	210					215					220				
Asn	Val	Leu	His	Arg	Arg	Pro	Asn	Lys	Lys	Lys	Ala	Lys	Val	Met	Arg
225					230					235					240
Leu	Ile	Phe	Val	Ile	Thr	Leu	Leu	Phe	Phe	Leu	Leu	Leu	Ala	Pro	Tyr
			245					250					255		
Tyr	Leu	Ala	Ala	Phe	Val	Ser	Ala	Phe	Glu	Asp	Val	Leu	Phe	Thr	Pro
		260					265					270			
Ser	Cys	Leu	Arg	Ser	Gln	Gln	Val	Asp	Leu	Ser	Leu	Met	Ile	Thr	Glu
		275					280					285			
Ala	Leu	Ala	Tyr	Thr	His	Cys	Cys	Val	Asn	Pro	Val	Ile	Tyr	Val	Phe
	290					295					300				
Val	Gly	Lys	Arg	Phe	Arg	Lys	Tyr	Leu	Trp	Gln	Leu	Phe	Arg	Arg	His
305					310					315					320
Thr	Ala	Ile	Thr	Leu	Pro	Gln	Trp	Leu	Pro	Phe	Leu	Ser	Glu	Asp	Arg
			325					330					335		
Ala	Gln	Arg	Ala	Ser	Ala	Arg	Leu	Pro	Ser	Thr	Val	Glu	Ile	Glu	Thr
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Ser	Ala	Asp	Leu												
		355													

<210> 5
 <211> 68
 <212> PRT
 <213> Mus muscalis

<400> 5
 Arg Asn Met Thr Ser Ile Tyr Leu Phe Asn Leu Ala Ile Ser Asp Leu
 1 5 10 15
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 20 25 30
 Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly Phe Tyr
 35 40 45
 Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu Thr Ile
 50 55 60
 Asp Arg Tyr Leu
 65

<210> 6
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> VARIANT
 <222> (1)...(1)
 <223> Xaa at position 1 can be G or S or T or A or
 L or I or V or M or F or Y or W or C

<221> VARIANT
 <222> (2)...(2)
 <223> Xaa at position 2 can be G or S or T or A or
 N or P or D or E

 <221> VARIANT
 <222> (3)...(3)
 <223> Xaa at position 3 can not be E or D or
 P or K or R or H

 <223> Xaa at position 4 can
 be any amino acid

 <223> Xaa at position 5 can
 be any amino acid

 <221> VARIANT
 <222> (6)...(6)
 <223> Xaa at position 6 can be L or I or V or M or
 N or Q or G or A

 <223> Xaa at position 7 can
 be any amino acid

 <223> Xaa at position 8 can
 be any amino acid

 <221> VARIANT
 <222> (9)...(9)
 <223> Xaa at position 9 can be L or I or V or M or
 F or T

 <221> VARIANT
 <222> (10)...(10)
 <223> Xaa at position 10 can be G or S or T or A or
 N or C

 <221> VARIANT
 <222> (11)...(11)
 <223> Xaa at position 11 can be L or I or V or M
 or F or Y or W or S or T or A or C

 <221> VARIANT
 <222> (12)...(12)
 <223> Xaa at position 12 can be D or E or N or H

 <221> VARIANT
 <222> (14)...(14)
 <223> Xaa at position 14 can be F or Y or W or C
 or S or H

 <223> Xaa at position 15
 can be any amino acid

 <223> Xaa at position 16
 can be any amino acid

 <221> VARIANT
 <222> (17)...(17)
 <223> Xaa at position 17 can be L or I or V or M

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 1 5 10 15
 Xaa